

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> RuvB Polypeptides and Uses Thereof

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<151> 1999-07-16

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Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala	
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Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met
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att cgc cag aag aag atg gcc ggc cgc gcg gtg ctc ctt gcg ggt ccg 306
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Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val
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Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala
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155 160 165

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170 175 180

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 425 430 435

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 Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln Gln Glu Arg Tyr Ile Thr
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 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
 145 150 155 160
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 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
 180 185 190
 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
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 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro
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 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
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His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
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 260 265 270
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
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 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
 290 295 300
 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
 305 310 315 320
 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
 325 330 335
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 340 345 350
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 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp
 370 375 380
 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
 385 390 395 400
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 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
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 Met Arg Ile Glu Glu Val Gln Ser Thr Ser
 1 5 10
 aag aag cag cgc atc gcc acc cac act cac atc aag ggc ctc ggc ctc 159
 Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly Leu
 15 20 25
 gac gcc aat gga atg tcg atg ccg ttg gcg gcg ggg ttc gtg ggc cag 207
 Asp Ala Asn Gly Met Ser Met Pro Leu Ala Ala Gly Phe Val Gly Gln
 30 35 40
 gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg atc cgc cag 255
 Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln
 45 50 55

aag aag atg gcc ggt cgc gcg ctg ctc ctt gcg ggc ccg ccc gcc acg Lys Lys Met Ala Gly Arg Ala Leu Leu Leu Ala Gly Pro Pro Ala Thr 60 65 70	303
ggc aaa acg gcg cta gcg ctc ggc ata gcg cag gag ctc ggc agc aag Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys 75 80 85 90	351
gtc cca ttc tgt cct atg gta gga tca gaa gtg tac tcc tca gag gtc Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu Val 95 100 105	399
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cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt att gaa ctt Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Ile Glu Leu 125 130 135	495
tcc cca gaa gag gct gag agc aca act ggt gga tat gcg aaa agc att Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile 140 145 150	543
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cct gcc agc gtg gtc gca aag acc aac ggg aga gaa aag atg tgc aag Pro Ala Ser Val Val Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys 415 420 425	1359
gct gac ctc gag gaa gtc agc ggg ctc tat ttg gat gcc aaa tcc tcg Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser 430 435 440	1407
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Met	Pro	Leu	Ala	Ala	Gly	Phe	Val	Gly	Gln	Ala	Ala	Ala	Arg	Glu	Ala			
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Ala	Gly	Leu	Ala	Val	Asp	Met	Ile	Arg	Gln	Lys	Lys	Met	Ala	Gly	Arg			
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Val	Gly	Ser	Glu	Val	Tyr	Ser	Ser	Glu	Val	Lys	Lys	Thr	Glu	Val	Leu			
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Met	Glu	Asn	Phe	Arg	Arg	Ala	Ile	Gly	Leu	Arg	Ile	Lys	Glu	Asn	Lys			
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Glu	Val	Tyr	Glu	Gly	Glu	Val	Ile	Glu	Leu	Ser	Pro	Glu	Glu	Ala	Glu			
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Ser	Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	Ile	Ser	His	Val	Ile	Ile	Gly			
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Leu	Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	Leu	Lys	Leu	Asp	Pro	Ser	Ile			
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Phe	Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro			
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Glu	Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	Val	Val	Asn	Arg	Tyr	Ile	Asp			
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Asn	Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	Pro	His	Gly	Ile	Pro	Val	Asp			
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Glu	Met	Ile	Gln	Ile	Leu	Ala	Ile	Arg	Ala	Gln	Val	Glu	Glu	Ile	Asp			
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Ile	Asp	Glu	Glu	Ser	Leu	Ala	Tyr	Leu	Gly	Glu	Ile	Gly	Gln	Gln	Thr			
385					390					395					400			
Ser	Leu	Arg	His	Ala	Ile	Gln	Leu	Leu	Ser	Pro	Ala	Ser	Val	Val	Ala			
				405					410					415				
Lys	Thr	Asn	Gly	Arg	Glu	Lys	Met	Cys	Lys	Ala	Asp	Leu	Glu	Glu	Val			

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 gcagctctag agagaacaga gagcgcataa ctacgcggcg cggcg atg agg ata gag 177
 Met Arg Ile Glu
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 gag gtg caa tcg acc tcg aag aag cag cgc atc gcc acc cac act cac 225
 Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile Ala Thr His Thr His
 5 10 15 20

 atc aag ggc ctc ggc ctc gac cag gcc aat gga atg tcg atg ccg ttg 273
 Ile Lys Gly Leu Gly Leu Asp Gln Ala Asn Gly Met Ser Met Pro Leu
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 gcg gcg ggg ttc gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg 321
 Ala Ala Gly Phe Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu
 40 45 50

 gcg gtc gac atg atc cgc cag aag aag atg gcc ggt cgc gcg ctg ctc 369
 Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg Ala Leu Leu
 55 60 65

 ctt gcg ggc ccg ccc gcc acg ggc aaa acg gcg cta gcg ctc ggc ata 417
 Leu Ala Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile
 70 75 80

 gcg cag gag ctc ggc agc aag gtc cca ttc tgt cct atg gta gga tca 465
 Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met Val Gly Ser
 85 90 95 100

 gaa gtg tac tcc tca gag gtc aag aaa act gag gtg ctg atg gaa aat 513
 Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu Met Glu Asn
 105 110 115

 ttc cgt aga gct ata ggt ttg cgt ata aag gaa aac aaa gag gtt tat 561
 Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr
 120 125 130

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gaa agt ctt gct tat tta ggc gag atc gga cag cag aca tct ttg aga Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg 390 395 400			1377
cat gct att cag ttg cta tca cct gcc agc gtg gtc gca aag acc aac His Ala Ile Gln Leu Leu Ser Pro Ala Ser Val Val Ala Lys Thr Asn 405 410 415 420			1425
ggg aga gaa aag atg tgc aag gct gac ctc gag gaa gtc agc ggg ctc Gly Arg Glu Lys Met Cys Lys Ala Asp Leu Glu Glu Val Ser Gly Leu 425 430 435			1473
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aga tac atc acc tagacttgca tctcctgctg tggaaggaaa agcctcgaag Arg Tyr Ile Thr 455			1573
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130		135		140
Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile				
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Gly Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Pro Ser				160
	165		170	175
Ile Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile				
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Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp				
	195		200	205
Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile				
	210		215	220
Pro Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr				240
225		230		235
Leu His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp				255
	245		250	
Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile				
	260		265	270
Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile				
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Asp Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu				
	290		295	300
Val His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu				
305		310		315
Glu Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile				320
	325		330	335
Cys Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val				
	340		345	350
Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro				
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Thr Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile				
	370		375	380
Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln				
385		390		395
Thr Ser Leu Arg His Ala Ile Gln Leu Leu Ser Pro Ala Ser Val Val				
	405		410	415
Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys Ala Asp Leu Glu Glu				
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Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln				
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<212> DNA

<213> Zea mays

<220>

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108

Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile

1

5

10

15

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gcg att gcg ttg gcg gcg ggg ttc gtg ggc cag aag aag atg gcc ggc Ala Ile Ala Leu Ala Ala Gly Phe Val Gly Gln Lys Lys Met Ala Gly	204
35 40 45	
cgc gcg gtg ctc ctt gcg ggt ccg ccc gcc acg ggc aag acg gcg cta Arg Ala Val Leu Leu Ala Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu	252
50 55 60	
gcg ggc ata gcc cag gag ctc ggc agc aag gtc cct ttc tgt cct atg Ala Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met	300
65 70 75	
gta gga tca gaa gtg tac tcc tcg gag gtc aag aaa act gag gtg ctg Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu	348
80 85 90 95	
atg gaa aat ttc cgt aga gct ata ggt ttg cgt ata aag gaa aac aaa Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys	396
100 105 110	
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115 120 125	
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130 135 140	
tta aag act gtt aaa ggg act aag caa ctg aag tta gat tct tca att Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile	540
145 150 155	
tat gat gct ctg atc aag gaa aag gtg gca gtg ggt gat gtt ata tac Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr	588
160 165 170 175	
atc gaa gca aat agt gga gca gtg aaa aga gtt ggt aga tgt gat tct Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser	636
180 185 190	
ttt gct aca gaa tac gat ctt gaa gct gaa gag tat gtt cct atc ccc Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro	684
195 200 205	
aaa ggt gaa gtc cat aag aaa aaa gaa att gtg cag gat gtc aca ctt Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu	732
210 215 220	
cat gac ctt gat gca gca aat gct cag cca caa ggt ggc caa gat att His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile	780
225 230 235	

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Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr	
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Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp	
260 265 270	
gaa gga att gca gag ctt gta cct ggt gtt ttg ttc att gat gag gtc	924
Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val	
275 280 285	
cac atg ttg gat atc gaa tgt ttt tct tat ctt aac cgt gca ttg gag	972
His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu	
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Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp	
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Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr	
340 345 350	
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Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp	
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Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val	
400 405 410 415	
agt ggg ctc tat ttg gat gcc aaa tcc tcg gct cgg ctg ctc cag gag	1356
Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu	
420 425 430	
caa caa gaa aga tac atc acc tagatttggg tcacctgtcg tggaagtctc	1407
Gln Gln Glu Arg Tyr Ile Thr	
435	
gaagagaatg tagttgccag ctcgaaagtc atctagtga ttgatctgct tcacaggtct	1467
tgagcgagc acatttcggg ggggacggct tgaattttgc agtgccctgct tgtgttagtc	1527
tccagagaag acttggtacc ggcatattgc ctgttcacgc actgttcgct gattagattg	1587

gtcaccggtg	caggaattgc	cgtgtgtgtt	ttttatcttg	ctcatcgggtg	tccggaatct	1647
gtgcctccac	gggttgatt	ggcccgaacc	ctatctttgt	aaccatggat	aatggatagc	1707
attcttacag	aatgcaactt	gcatggcttt	attatcttcta	aatgtccata	aagcttaaca	1767
aaatgtttct	acaacatata	gacctcctgc	ccaaattaaa	attcgtttta	gcttagataa	1827
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<210> 10

<211> 438

<212> PRT

<213> Zea mays

<400> 10

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			20					25					30		
Ile	Ala	Leu	Ala	Ala	Gly	Phe	Val	Gly	Gln	Lys	Lys	Met	Ala	Gly	Arg
		35					40					45			
Ala	Val	Leu	Leu	Ala	Gly	Pro	Pro	Ala	Thr	Gly	Lys	Thr	Ala	Leu	Ala
	50					55					60				
Gly	Ile	Ala	Gln	Glu	Leu	Gly	Ser	Lys	Val	Pro	Phe	Cys	Pro	Met	Val
65				70					75					80	
Gly	Ser	Glu	Val	Tyr	Ser	Ser	Glu	Val	Lys	Lys	Thr	Glu	Val	Leu	Met
				85					90					95	
Glu	Asn	Phe	Arg	Arg	Ala	Ile	Gly	Leu	Arg	Ile	Lys	Glu	Asn	Lys	Glu
			100					105					110		
Val	Tyr	Glu	Gly	Glu	Val	Thr	Glu	Leu	Ser	Pro	Glu	Glu	Ala	Glu	Ser
		115					120					125			
Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	Ile	Ser	His	Val	Ile	Ile	Ser	Leu
	130					135					140				
Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	Leu	Lys	Leu	Asp	Ser	Ser	Ile	Tyr
145					150					155				160	
Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	Ala	Val	Gly	Asp	Val	Ile	Tyr	Ile
				165					170					175	
Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	Arg	Val	Gly	Arg	Cys	Asp	Ser	Phe
		180						185					190		
Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro	Lys
		195					200					205			
Gly	Glu	Val	His	Lys	Lys	Lys	Glu	Ile	Val	Gln	Asp	Val	Thr	Leu	His
	210					215					220				
Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	Pro	Gln	Gly	Gly	Gln	Asp	Ile	Leu
225					230					235				240	
Ser	Leu	Met	Gly	Gln	Met	Met	Lys	Pro	Arg	Lys	Thr	Glu	Ile	Thr	Glu
				245					250					255	
Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	Val	Val	Asn	Arg	Tyr	Ile	Asp	Glu
			260					265					270		
Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	Val	Leu	Phe	Ile	Asp	Glu	Val	His
		275					280					285			
Met	Leu	Asp	Ile	Glu	Cys	Phe	Ser	Tyr	Leu	Asn	Arg	Ala	Leu	Glu	Ser
	290					295					300				
Pro	Leu	Ser	Pro	Ile	Val	Ile	Leu	Ala	Thr	Asn	Arg	Gly	Ile	Cys	Asn
305					310					315				320	
Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	Pro	His	Gly	Ile	Pro	Val	Asp	Leu
				325					330					335	
Leu	Asp	Arg	Leu	Val	Ile	Ile	Arg	Thr	Glu	Thr	Tyr	Gly	Pro	Thr	Glu
			340					345					350		

Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp Met
 355 360 365
 Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser
 370 375 380
 Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser Lys
 385 390 395 400
 Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val Ser
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 420 425 430
 Gln Glu Arg Tyr Ile Thr
 435

<210> 11

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 11

tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa

36